

SEQUENCE LISTING

<110> Allen, Steve
Kinney, Tony
Miao, Gou-Hua
Orozco, Buddy

<120> PLANT BIOTIN SYNTHASE

<130> BB1429 US NA

<140>

<141>

<150> 60/172929

<151> December 21, 1999

<160> 36

<170> Microsoft Office 97

<210> 1

<211> 512

<212> DNA

<213> Hordeum vulgare

<220>

<221> unsure

<222> (94)

<220>

<221> unsure

<222> (460)

<220>

<221> unsure

<222> (462)

<400> 1

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cgcctccgcc gttagcgccg cgcccttctc atcggtatcg gcggccgcgg cggaggcgga 180
cgggcgggtgc gggacgggccc caggaacgac tggaccgcgc ccgagatcca ggccatctac 240
gactccccgc tcctcgacct cctcttccac ggggctcaag tccataggaa tgtccataaa 300
tttagagaag tgcaacaatg cacacttctt tcaataaaga ctggtgggtg cagcgaagat 360
tgttcatact gcccacagtc ttcaagatac agtaccggat tgaaggctga aaaattaatg 420
aagaaagatg ccgtcctaga agcagctaaa aaggcaaagn angctgggag cacccgattt 480
tgattggagc gatggagaga gacaattggc ag 512
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<210> 2

<211> 137

<212> PRT

<213> Hordeum vulgare

<220>

<221> UNSURE

<222> (131)


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aactgcattg gagaaa                                         496

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<210> 4
<211> 102
<212> PRT
<213> Zea mays

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<220>
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<222> (48)..(49)

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<220>
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<222> (64)

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<220>
<221> UNSURE
<222> (91)

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<400> 4
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
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Pro Leu Ala Ala Ala Ala Gly Phe Ser Ser Ala Ala Ala Glu Ala Glu
          20             25             30
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa
      35             40             45
Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa
    50             55             60
Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Met Asn
 65             70             75             80
Lys Tyr Ala Val Leu Gly Ala Ala Lys Lys Xaa Lys Glu Ser Gly Lys
          85             90             95

Gln Pro Phe Leu His Gly
      100

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<210> 5
<211> 497
<212> DNA
<213> Zea mays

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<220>
<221> unsure
<222> (192)

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<220>
<221> unsure
<222> (460)

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<220>
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<222> (463)

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<220>
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 <222> (490)

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 cgccgcccgc gngttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc 240
 gcggaacgac tggagccggc ccgagattca agccgtctac gactcaccgc tcctcgacct 300
 cctctttcac ggggctcaag tccacagaaa tgtccataaa ttcaagagaa gtgcagcaat 360
 gcacacttct ttcaatcaag actggtggga tgcagtgaag attgttctta ctgtcctcaa 420
 gtcatacaag aatacaacac tgggattgaa gggcccaaan aanttgatna aaaaagatg 480
 ctgtcttggg aacaaca 497

<210> 6
 <211> 98
 <212> PRT
 <213> Zea mays

<220>
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 <222> (23)

<220>
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 <222> (72)

<220>
 <221> UNSURE
 <222> (89)

<400> 6
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 1 5 10 15
 Pro Leu Ala Ala Ala Ala Xaa Phe Ser Ser Ala Ala Ala Glu Ala Glu
 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Xaa Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln

<210> 7
 <211> 1152

<212> DNA
 <213> Zea mays

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 ggccttgatg ctgctagcgc gcaacctgcg ctcccgcctc cgcccaccgc tcgccgcgcg 180
 cgcggcggtc tcgtcggccg cggcggaggc ggagagggcg atacgggacg ggccgcggaa 240
 cgactggagc cggcccgaga tccaggccgt ctacgactca ccgctcctcg acctcctctt 300
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 atacaacact ggattgaagg cccaaaaatt gatgaacaaa tatgctgtct tggaagcagc 480
 aaaaaaggca aaagagtctg ggagcaccgc tttttgcatg ggagctgcat ggagagaaac 540
 cattggcagg aatcaaacat tcaaccagat tcttgaatat gtcaaggaaa taaggggtat 600
 gggcatggag gtctgttgca cactaggcat gatagagaaa caacaagctg aagaactcaa 660
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 cattattacc acaagatcat atgatgatag actgcagact cttgagcatg tccgtgaagc 780
 tggaataagc atctgctcag gtggaatcat tgggtcttggg gaagcagagg aggaccgggt 840
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 gatgttcaag at 1152

<210> 8
 <211> 344
 <212> PRT
 <213> Zea mays

<400> 8
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 1 5 10 15
 Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
 100 105 110
 Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
 115 120 125
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
 130 135 140
 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
 145 150 155 160

Met	Gly	Met	Glu	Val	Cys	Cys	Thr	Leu	Gly	Met	Ile	Glu	Lys	Gln	Gln	
				165					170					175		
Ala	Glu	Glu	Leu	Lys	Lys	Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Leu	
				180					185					190		
Asp	Thr	Ser	Arg	Glu	Tyr	Tyr	Pro	Asn	Ile	Ile	Thr	Thr	Arg	Ser	Tyr	
				195					200					205		
Asp	Asp	Arg	Leu	Gln	Thr	Leu	Glu	His	Val	Arg	Glu	Ala	Gly	Ile	Ser	
				210					215					220		
Ile	Cys	Ser	Gly	Gly	Ile	Ile	Gly	Leu	Gly	Glu	Ala	Glu	Glu	Asp	Arg	
				225					230					235		
Val	Gly	Leu	Leu	His	Thr	Leu	Ala	Thr	Leu	Pro	Thr	His	Pro	Glu	Ser	
				245					250					255		
Val	Pro	Ile	Asn	Ala	Leu	Val	Ala	Val	Lys	Gly	Thr	Pro	Leu	Glu	Asp	
				260					265					270		
Gln	Lys	Pro	Val	Glu	Ile	Trp	Glu	Met	Ile	Arg	Met	Ile	Ala	Thr	Ala	
				275					280					285		
Arg	Ile	Thr	Met	Pro	Lys	Ala	Met	Val	Arg	Leu	Ser	Ala	Gly	Arg	Val	
				290					295					300		
Arg	Phe	Ser	Met	Pro	Glu	Gln	Ala	Leu	Cys	Phe	Leu	Ala	Gly	Ala	Asn	
				305					310					315		
Ser	Ile	Leu	Ala	Gly	Glu	Lys	Leu	Leu	Thr	Thr	Ala	Asn	Asn	Asp	Phe	
				325					330					335		
Asp	Ala	Asp	Gln	Ala	Met	Phe	Lys									
				340												

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<210> 9
<211> 562
<212> DNA
<213> Argemone mexicana
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gagagctcgt	cttcgacctt	tgattttcat	ttctacattt	tcttctctct	catcatcttc	180	
ttcttcttca	gctgctgctg	ttcaagcaga	agaacgatt	aaagaagggtc	caagaaacga	240	
ttggagcaga	gatgaaatta	aatcggttta	tgattctcca	gttctcgatc	ttctcttcca	300	
tgcagctcaa	gtccatagac	atgctcacaa	cttcagggaa	gtgcagcaat	gtactcttct	360	
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tgacactgga	gtgaaagccc	aaaagctgat	gaacaaggga	cgcagttctg	caaggaagca	480	
agaaaaggca	aaggaggcgg	ggtagtacac	gttttcgcaa	tggtggctgc	aatggggaga	540	
tacaatgggg	aanqaagaac	aa				562	

<212> PRT
 <213> Argemone mexicana

<400> 10
 Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe
 1 5 10 15
 Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ser Ala Ala
 20 25 30
 Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
 35 40 45
 Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
 50 55 60
 Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
 65 70 75 80
 Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
 85 90 95
 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
 100 105 110
 Ala Gln Lys Leu Met Asn Lys
 115

<210> 11
 <211> 1340
 <212> DNA
 <213> Glycine max

<400> 11
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 tctcaccata aactccaaag tcccaacgct aaacgaaacc aaaccccaaa cacaatatcc 120
 gttgttgtct gttgtctctg tcgtgtctat attcgcagat ctctcactca ttctctgttg 180
 tttctctgcc caacttcgaa ttcgaaagca aaaacatggt tttggcgaga cccattttcc 240
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 caattcaagc tgagagagcc atcaaagaag gaccagaaaa cgattggagc cgagaccaag 360
 tcaaatccat ctacgactct cccattctcg atcttctctt ccatggggct caagttcaca 420
 gacatgctca taacttcagg gaagttcaac agtgtactct tctgtctatc aaaacaggag 480
 ggtgcagtga agattgttcc tattgtcctc aatcctctaa gtatgataca ggagtcaaaa 540
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 ggagcactcg cttttgtatg ggtgctgctg ggaggggatac actaggaaga aagaccaact 660
 tcaaccagat ccttgaatat gtgaaagaca taagggacat ggggaatggag gtttggtgca 720
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 cccctcttga ggatcagaag cctgttgaaa tatgggagat gattcgcagt atagcaactg 1080
 cacgtatcgt aatgccaaaa gcaatggtea gggtatcagc tggcagagtt cgattctcca 1140
 tgcttgagca ggcattgtgc tttcttgctg gtgcaaatc tatattcact ggtgaaaagc 1200
 ttctcactac tcctaacaat gattttgatg ctgatcaact catgtttaaa gttcttggac 1260
 ttctcccaaa agctccaagc ttacatgaag gtgaaactag tgtgacagaa gattataagg 1320
 aagcagcttc ttctagttga 1340

<210> 12
 <211> 374

<212> PRT
 <213> Glycine max

<400> 12

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Met Phe Leu Ala Arg Pro Ile Phe Arg Ala Pro Ser Leu Trp Ala Leu
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His Ser Ser Tyr Ala Tyr Ser Ser Ala Ser Ala Ala Ala Ile Gln Ala
      20           25           30

Glu Arg Ala Ile Lys Glu Gly Pro Arg Asn Asp Trp Ser Arg Asp Gln
      35           40           45

Val Lys Ser Ile Tyr Asp Ser Pro Ile Leu Asp Leu Leu Phe His Gly
      50           55           60

Ala Gln Val His Arg His Ala His Asn Phe Arg Glu Val Gln Gln Cys
      65           70           75           80

Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr
      85           90           95

Cys Pro Gln Ser Ser Lys Tyr Asp Thr Gly Val Lys Arg Pro Ser Leu
      100          105          110

Met Asn Lys Glu Ala Val Leu Gln Ala Ala Lys Lys Ala Lys Glu Ala
      115          120          125

Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Thr Leu Gly
      130          135          140

Arg Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg
      145          150          155          160

Asp Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln
      165          170          175

Gln Ala Val Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn
      180          185          190

Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Thr
      195          200          205

Tyr Asp Glu Arg Leu Gln Thr Leu Glu Phe Val Arg Asp Ala Gly Ile
      210          215          220

Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp
      225          230          235          240

Arg Val Gly Leu Leu His Thr Leu Ser Thr Leu Pro Thr His Pro Glu
      245          250          255

Ser Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu
      260          265          270

Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr
      275          280          285

Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg
      290          295          300

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Val Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala
 305 310 315 320

Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr Pro Asn Asn Asp
 325 330 335

Phe Asp Ala Asp Gln Leu Met Phe Lys Val Leu Gly Leu Leu Pro Lys
 340 345 350

Ala Pro Ser Leu His Glu Gly Glu Thr Ser Val Thr Glu Asp Tyr Lys
 355 360 365

Glu Ala Ala Ser Ser Ser
 370

<210> 13
 <211> 479
 <212> DNA
 <213> Glycine max

<400> 13
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 actcgacact atctcttctt ctgttcgtct tcaagttcaa aagtcgagaa actatgggtac 120
 cgtatcatct gttcctcctc aagctacaga aacatcaagc acatcaccta gtaaggatgt 180
 ctaccaagaa gcactcaacg caactgaacc ccgcagcaat tggacaagag aagaaatcaa 240
 ggcgatctat gataagccat tgatggagtt atgttggggg gctggtagtt tgcacaggaa 300
 attccatata cctgggggcta ttcagatgtg tacattgttg aacatcaaga cgggtggttg 360
 ctggaggagg ttgttcttac tggcgcccaa tcatcccgct accaaaccgg tctcaaagcc 420
 ctcaaaaaat ggtcctccgt cgaatctgtc ctgcgaagcc gcccgcgcat gccaaaaga 479

<210> 14
 <211> 52
 <212> PRT
 <213> Glycine max

<400> 14
 Arg Ser Asn Trp Thr Arg Glu Glu Ile Lys Ala Ile Tyr Asp Lys Pro
 1 5 10 15

Leu Met Glu Leu Cys Trp Gly Ala Gly Ser Leu His Arg Lys Phe His
 20 25 30

Ile Pro Gly Ala Ile Gln Met Cys Thr Leu Leu Asn Ile Lys Thr Gly
 35 40 45

Gly Cys Ser Glu
 50

<210> 15
 <211> 589
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (321)

<220>
 <221> UNSURE
 <222> (69)

<400> 16
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 1 5 10 15

Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
 20 25 30

Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
 35 40 45

Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
 50 55 60

Glu Leu Gln Glu Xaa Asp Phe Thr Ala Tyr Asn His Asn Leu
 65 70 75

<210> 17
 <211> 1396
 <212> DNA
 <213> Hordeum vulgare

<400> 17
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 ccccttcgc ctccgcggtt agcgccgcgc ccttctcatc ggtatcggcg gccgcggcgg 180
 aggcggagcg ggcggtgcgg gacggggcca ggaacgactg gaccgcgcc gagatccagg 240
 ccatctacga ctccccgctc ctcgacctcc tcttccacgg ggctcaagtc cataggaatg 300
 tccataaatt tagagaagtg caacaatgca cacttctttc aataaagact ggtgggtgca 360
 gcgaagattg ttcatactgc ccacagtctt caagatacag taccggattg aaggctgaaa 420
 aattaatgaa gaaagatgcc gtcctagaag cagctaaaaa ggcaaaggag gctgggagca 480
 cccgattttg catgggagcc gcatggagag agacaattgg caggaaaaca aacttcaacc 540
 agattcttga atagtcaag gacataagag gtatgggcat ggaggtctgt tgcaccctgg 600
 gcatgctaga gaaacagcaa gctgaagaac tcaagaaggc tggacttaca gcttataatc 660
 ataacctaga tacatcaaga gaatattacc cgaacattat ttctacaaga tcgtatgatg 720
 atagattaca gactcttcag catgtccgtg aagctggaat aagcgtctgc tcaggtggaa 780
 ttattgggtct tggagaggcg gaggaagacc gtgtagggct gttgcataca ctggccactt 840
 tgccaacaca cccagagagt gttcctatca atgcattgat tgctgtcaaa ggcacgcctc 900
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 ctggcaccat tatctccagc tagagctttg tactgtaggg atcatgatat tttgtactcc 1320
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<210> 18
 <211> 405
 <212> PRT
 <213> Hordeum vulgare

<400> 18
 Thr Thr Thr Pro Ser Ala Val Ser Pro Ser Ala Ala Ala Pro Phe
 1 5 10 15

Arg Pro Ala Leu Leu Ala Glu Pro Ala Met Met Leu Leu Leu Ala Arg
 20 25 30
 Ser Leu Arg Ser Arg Val Arg Ser Pro Phe Ala Ser Ala Val Ser Ala
 35 40 45
 Ala Pro Phe Ser Ser Val Ser Ala Ala Ala Ala Glu Ala Glu Arg Ala
 50 55 60
 Val Arg Asp Gly Pro Arg Asn Asp Trp Thr Arg Pro Glu Ile Gln Ala
 65 70 75 80
 Ile Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala Gln Val
 85 90 95
 His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr Leu Leu
 100 105 110
 Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln
 115 120 125
 Ser Ser Arg Tyr Ser Thr Gly Leu Lys Ala Glu Lys Leu Met Lys Lys
 130 135 140
 Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr
 145 150 155 160
 Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
 165 170 175
 Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
 180 185 190
 Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
 195 200 205
 Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr
 210 215 220
 Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr Asp Asp
 225 230 235 240
 Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser Val Cys
 245 250 255
 Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly
 260 265 270
 Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val Pro
 275 280 285
 Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp Gln Lys
 290 295 300
 Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala Arg Ile
 305 310 315 320
 Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe
 325 330 335

Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile
340 345 350

Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp Ala
355 360 365

Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro Asn
370 375 380

Phe Gly Asp Glu Glu Ala Thr Val Ala Ser Ser Thr Glu Arg Cys Glu
385 390 395 400

Gln Ala Ala Ser Met
405

<210> 19
<211> 1467
<212> DNA
<213> Zea mays

<400> 19

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cgcccgtgc	tcctctatcc	ctttcctgct	gctgctacta	ccttaagcta	tcactatcat	180
ggccttgatg	ctgctagcgc	gcaacctgcg	ctccgcctc	cgcccaccgc	tcgccgccgc	240
cgcggcgttc	tcgtcggccg	cggcggaggc	ggagagggcg	atacgggacg	ggccgcggaa	300
cgactggagc	cggccccgaga	tccaggccgt	ctacgactca	ccgctcctcg	acctcctctt	360
tcacggggct	cagtcatcaa	gatacaaac	tggattgaag	gccccaaaaat	tgatgaacaa	420
atatgctgtc	ttggaagcag	caaaaaaggc	aaaagagtct	gggagcacc	gtttttgcat	480
gggagctgca	tggagagaaa	ccattggcag	gaaatcaaac	ttcaaccaga	ttcttgaata	540
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atcaagagag	tattatccca	acattattac	cacaagatca	tatgatgata	gactgcagac	720
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tgcttcgatg	tagaatatat	acatatcatt	accgattatc	cgtatcacgg	ttggggcgaa	1260
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<210> 20
<211> 344
<212> PRT
<213> Zea mays

<400> 20

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Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
20 25 30

Arg	Ala	Ile	Arg	Asp	Gly	Pro	Arg	Asn	Asp	Trp	Ser	Arg	Pro	Glu	Ile
35						40						45			
Gln	Ala	Val	Tyr	Asp	Ser	Pro	Leu	Leu	Asp	Leu	Leu	Phe	His	Gly	Ala
50						55				60					
Gln	Ser	Ser	Arg	Tyr	Asn	Thr	Gly	Leu	Lys	Ala	Gln	Lys	Leu	Met	Asn
65				70						75				80	
Lys	Tyr	Ala	Val	Leu	Glu	Ala	Ala	Lys	Lys	Ala	Lys	Glu	Ser	Gly	Ser
				85				90						95	
Thr	Arg	Phe	Cys	Met	Gly	Ala	Ala	Trp	Arg	Glu	Thr	Ile	Gly	Arg	Lys
		100						105				110			
Ser	Asn	Phe	Asn	Gln	Ile	Leu	Glu	Tyr	Val	Lys	Glu	Ile	Arg	Gly	Met
		115				120						125			
Gly	Met	Glu	Val	Cys	Cys	Thr	Leu	Gly	Met	Ile	Glu	Lys	Gln	Gln	Ala
130						135				140					
Glu	Glu	Leu	Lys	Lys	Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Leu	Asp
145				150						155				160	
Thr	Ser	Arg	Glu	Tyr	Tyr	Pro	Asn	Ile	Ile	Thr	Thr	Arg	Ser	Tyr	Asp
				165				170						175	
Asp	Arg	Leu	Gln	Thr	Leu	Glu	His	Val	Arg	Glu	Ala	Gly	Ile	Ser	Ile
		180						185				190			
Cys	Ser	Gly	Gly	Ile	Ile	Gly	Leu	Gly	Glu	Ala	Glu	Glu	Asp	Arg	Val
		195				200						205			
Gly	Leu	Leu	His	Thr	Leu	Ala	Thr	Leu	Pro	Thr	His	Pro	Glu	Ser	Val
210						215				220					
Pro	Ile	Asn	Ala	Leu	Val	Ala	Val	Lys	Gly	Thr	Pro	Leu	Glu	Asp	Gln
225				230						235				240	
Lys	Pro	Val	Glu	Ile	Trp	Glu	Met	Ile	Arg	Met	Ile	Ala	Thr	Ala	Arg
				245				250						255	
Ile	Thr	Met	Pro	Lys	Ala	Met	Val	Arg	Leu	Ser	Ala	Gly	Arg	Val	Arg
		260						265				270			
Phe	Ser	Met	Pro	Glu	Gln	Ala	Leu	Cys	Phe	Leu	Ala	Gly	Ala	Asn	Ser
		275				280						285			
Ile	Phe	Ala	Gly	Glu	Lys	Leu	Leu	Thr	Thr	Ala	Asn	Asn	Asp	Phe	Asp
290						295				300					
Ala	Asp	Gln	Ala	Met	Phe	Lys	Ile	Leu	Gly	Leu	Ile	Pro	Lys	Ala	Pro
305				310						315				320	
Ser	Phe	Gly	Glu	Glu	Glu	Ala	Ser	Ala	Ala	Ala	Pro	Thr	Glu	Ser	Glu
				325				330						335	
Arg	Ser	Glu	Gln	Ala	Ala	Ser	Met								
		340													

<210> 21
 <211> 1515
 <212> DNA
 <213> Zea mays

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 ttaagctatc atggccttga tgctgctagc gcgcaacctg cgctcccgcc tccgcccacc 180
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 cgggcccggg aacgactgga gccggcccga gatccaggcc gtctacgact caccgctcct 300
 cgacctctc tttcacgggg ctcagggtcca cagaaatgtc cataaattca gagaagtgca 360
 gcaatgcaca cttcttttcaa tcaagactgg tggatgcagt gaagattggt cttactgtcc 420
 tcagtcatca agatacaaca ctggattgaa ggcccaaaaa ttgatgaaca aagatgctgt 480
 cttggaagca gcaaaaaagg caaaagagtc tgggagcacc cgtttttgca tgggagctgc 540
 atggagagaa accattggca ggaaatcaaa cttcaaccag attcttgaat atgtcaagga 600
 aataaggggt atgggcatgg aggtctgttg cacactaggc atgatagaga aacaacaagc 660
 tgaagaactc aagaaggctg gacttacagc atataatcat aacctagata catcaagaga 720
 gtattatccc aacattatta ccacaagatc atatgatgat agactgcaga ctcttgagca 780
 tgtccgtgaa gctggaataa gcatctgctc aggtggaatc attggtcttg gtgaagcaga 840
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 tccattaat gcattggttg ctgtaaaagg cacacctctt gaggaccaga agcctgtaga 960
 gatctgggaa atgatccgca tgatcgccac tgctcggatc acgatgccaa aggcaatggt 1020
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 ggaagaggtg tctgcggcgg ctcccgcaga atccgagagg tctgagcaag ctgcttcgat 1260
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 accgtttag ctagagcatt ggattgtaga aaccacaaca tttcattatt ttgtaattgc 1380
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 aaaaaaaaaa aaaaaa 1515

<210> 22
 <211> 377
 <212> PRT
 <213> Zea mays

<400> 22
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 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
 100 105 110

Asn Lys Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
 115 120 125
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
 130 135 140
 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
 145 150 155 160
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
 165 170 175
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
 180 185 190
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
 195 200 205
 Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
 210 215 220
 Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
 225 230 235 240
 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
 245 250 255
 Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp
 260 265 270
 Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
 275 280 285
 Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
 290 295 300
 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
 305 310 315 320
 Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
 325 330 335
 Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
 340 345 350
 Pro Ser Phe Gly Glu Glu Glu Val Ser Ala Ala Ala Pro Ala Glu Ser
 355 360 365
 Glu Arg Ser Glu Gln Ala Ala Ser Met
 370 375

<210> 23
 <211> 1439
 <212> DNA
 <213> Zea mays

<400> 23
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 ttgatgctgc tagcgcgcaa cctgcgctcc cgcctccgcc caccgctcgc cgccgccgcg 180


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ggggctcagg tccacagaaa tgtccataaa ttccagagaag tgcagcaatg cacacttctt 360
tcaatcaaga ctggtggatg cagtgaagat tgttcttact gtctcagtc atcaagatac 420
aacactggat tgaaggccca aaaattgatg aacaaatatg ctgtcttggg agcagcaaaa 480
aaggcaaaag agtctgggag caccggtttt tgcatgggag ctgcatggag agaaaccatt 540
ggcaggaaat caaacttcaa ccagattctt gaatatgtca aggaaataag gggtagggc 600
atggaggtct gttgcacact aggcattgata gagaaacaac aagctgaaga actcaagaag 660
gctggactta cagcatataa tcataaccta gatacatcaa gagagtatta tcccaacatt 720
attaccacaa gatcatatga tgatagactg cagactcttg agcatgtccg tgaagctgga 780
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gttgctgtaa aaggcacacc tcttgaggac cagaagcctg tagagatctg ggaaatgatc 960
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cattggattg tagaaaccac aacatttcat tattttgtaa ttgcttgaga ctgaatgggg 1380
gatacccatg tcgggctaga tcaatggaca acttccacac aaaaaaaaaa aaaaaaaaaa 1439

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<210> 24
 <211> 377
 <212> PRT
 <213> Zea mays

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<400> 24
Met Ala Leu Met Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 1             5             10            15

Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
          20             25             30

Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
   35             40             45

Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
   50             55             60

Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
   65             70             75             80

Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
          85             90             95

Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
   100            105            110

Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
   115            120            125

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
   130            135            140

Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
   145            150            155            160

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
          165            170            175

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Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
180 185 190

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
195 200 205

Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
210 215 220

Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
225 230 235 240

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
245 250 255

Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp
260 265 270

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
275 280 285

Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
290 295 300

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
305 310 315 320

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
325 330 335

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
340 345 350

Pro Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser
355 360 365

Glu Arg Ser Glu Gln Ala Ala Ser Met
370 375

<210> 25

<211> 1477

<212> DNA

<213> Argemone mexicana

<400> 25

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catcttcttc	ttcttcagct	gctgctgttc	aagcagaaag	aacgattaaa	gaagggtccaa	240
gaaacgattg	gagcagagat	gaaattaaat	cggtttatga	ttctccagtt	ctcgatcttc	300
tcttccatgc	agctcaagtc	catagacatg	ctcacaactt	caggggaagtg	cagcaatgta	360
ctcttctctc	tgttaagaca	ggtgggtgca	gtgaagattg	ttcatattgt	ccacaatctt	420
ccaggatgta	cactggagtg	aaagcccaaa	agctgatgaa	caaggacgca	gttctgcagg	480
cagcagaaaa	ggcaaaggag	gcgggtagta	cacgtttctg	catgggtgct	gcatggagag	540
atacagtgga	caggaagacc	aacttcaaac	agatcctcga	atatgtaaaa	gaaattcggg	600
gtatgggaat	ggaggtatgc	tgcactttag	gcatgatcga	gaagcagcaa	gctgtggaac	660
tcaagcaggc	tgggctcaca	gcttacaatc	ataatcttga	tacttcaaga	gagtattacc	720
ctaacatcat	caccacaaga	tcttacgatg	agcgcttgga	aactcttcag	ttcgtccggg	780
aagcagggat	caatgtctgc	tcaggaggaa	taatagggct	aggagaagca	gaggaggatc	840

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gagttggtct tttgcataca ctagcaacgc ttccttcaca tccagaaaagt gttcccatca 900
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catcttttoga agccgagaga tgtgaacaag aagcaactgc gtcatagttc ttgcttcgat 1260
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acatgaagtt tctttgtatg aattatgaaa cctccaaaat aagctatact atttataaca 1380
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1477

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<210> 26
 <211> 379
 <212> PRT
 <213> Argemone mexicana

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<400> 26
Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe
  1              5              10              15

Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ser Ser Ala Ala
      20              25              30

Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
      35              40              45

Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
      50              55              60

Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
      65              70              75              80

Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
      85              90              95

Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
      100             105             110

Ala Gln Lys Leu Met Asn Lys Asp Ala Val Leu Gln Ala Ala Glu Lys
      115             120             125

Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
      130             135             140

Asp Thr Val Gly Arg Lys Thr Asn Phe Lys Gln Ile Leu Glu Tyr Val
      145             150             155             160

Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
      165             170             175

Ile Glu Lys Gln Gln Ala Val Glu Leu Lys Gln Ala Gly Leu Thr Ala
      180             185             190

Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile
      195             200             205

Thr Thr Arg Ser Tyr Asp Glu Arg Leu Glu Thr Leu Gln Phe Val Arg
      210             215             220

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Glu Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
 225 230 235 240
 Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro
 245 250 255
 Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
 260 265 270
 Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
 275 280 285
 Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
 290 295 300
 Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
 305 310 315 320
 Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
 325 330 335
 Pro Asn Asn Asp Phe Asp Ala Asp Gln Met Met Phe Lys Ile Leu Gly
 340 345 350
 Leu Thr Pro Lys Ala Pro Asn Phe Asp Gln Thr Ser Thr Ser Phe Glu
 355 360 365
 Ala Glu Arg Cys Glu Gln Glu Ala Thr Ala Ser
 370 375

<210> 27
 <211> 1526
 <212> DNA
 <213> Glycine max

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 taaacagtct caccataaac tccaaagtcc caacgctaaa cgaaaccaa ccccaaacac 120
 aaataccggt gttgtctggt gtctctgtcg tgtctatatt cgcagatctc tcactcattc 180
 tctgtttggt ctctgcccac cttcgaattc gaaagcaaaa acatgttttt ggcgagacc 240
 attttccgag caccctccct ttgggcgttg cactcttcc acgcgtattc ctctgcctca 300
 gcagctgcaa ttcaagctga gagagccatc aaagaaggac ccagaaacga ttggagccga 360
 gaccaagtca aatccatcta cgactctccc attctcgatc ttctcttcca tggggctcaa 420
 gttcacagac atgctcataa cttcagggaa gttcagcagt gtactcttct gtctatcaaa 480
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 gaggctggga gcactcgctt ttgtatgggt gctgcatgga gggatacact gggaagaaag 660
 accaacttca accagatcct tgaatatgtg aaagacataa gggacatggg aatggaggtt 720
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 tgttctggag gaattatagg gcttgagaa gcagaggagg atcgtgtagg tttgttacat 960
 acattgtcaa cacttcccac ccatccagag agtggtccta ttaatgcact tgttgctgta 1020
 aaggaacccc ctcttgagga tcagaagcct gttgaaatat gggagatgat tcgcatgata 1080
 gcaactgcac gtatcgtaat gccaaaagca atggtcagggt tatcagctgg cagagttcga 1140
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 gaaaagcttc tcaactactc taacaatgat tttgatgctg atcaactcat gtttaaagtt 1260
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 tataaggaag cagcttcttc tagttgagtt gtcaacgggt tcaaaacaat atctgtgatc 1380
 cttcaacttc totaattgct cattagcatg tactgatggt aggtttcatt gaatttgtct 1440

aatctcagct ttgaagacac aaactccaac acttaaaaat aaatattgaa attattgatt 1500
 tttccctaaa aaaaaaaaaa aaaaaa 1526

<210> 28
 <211> 415
 <212> PRT
 <213> Glycine max

<400> 28
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 35 40 45
 Phe Arg Ala Pro Ser Leu Trp Ala Leu His Ser Ser Tyr Ala Tyr Ser
 50 55 60
 Ser Ala Ser Ala Ala Ala Ile Gln Ala Glu Arg Ala Ile Lys Glu Gly
 65 70 75 80
 Pro Arg Asn Asp Trp Ser Arg Asp Gln Val Lys Ser Ile Tyr Asp Ser
 85 90 95
 Pro Ile Leu Asp Leu Leu Phe His Gly Ala Gln Val His Arg His Ala
 100 105 110
 His Asn Phe Arg Glu Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr
 115 120 125
 Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln Ser Ser Lys Tyr
 130 135 140
 Asp Thr Gly Val Lys Gly Gln Arg Leu Met Asn Lys Glu Ala Val Leu
 145 150 155 160
 Gln Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met
 165 170 175
 Gly Ala Ala Trp Arg Asp Thr Leu Gly Arg Lys Thr Asn Phe Asn Gln
 180 185 190
 Ile Leu Glu Tyr Val Lys Asp Ile Arg Asp Met Gly Met Glu Val Cys
 195 200 205
 Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Val Glu Leu Lys Lys
 210 215 220
 Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr
 225 230 235 240
 Tyr Pro Asn Ile Ile Thr Thr Arg Thr Tyr Asp Glu Arg Leu Gln Thr
 245 250 255
 Leu Glu Phe Val Arg Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile
 260 265 270

Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr
275 280 285

Leu Ser Thr Leu Pro Thr His Pro Glu Ser Val Pro Ile Asn Ala Leu
290 295 300

Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile
305 310 315 320

Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys
325 330 335

Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe Ser Met Pro Glu
340 345 350

Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu
355 360 365

Lys Leu Leu Thr Thr Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met
370 375 380

Phe Lys Val Leu Gly Leu Leu Pro Lys Ala Pro Ser Leu His Glu Gly
385 390 395 400

Glu Thr Ser Val Thr Glu Asp Tyr Lys Glu Ala Ala Ser Ser Ser
405 410 415

<210> 29
<211> 1659
<212> DNA
<213> Glycine max

<400> 29
aaagagtgtgta tacagataga tttccaaact ccactcactc accactatgg cgactctcag 60
aacttcccta tcacgatccc tcatcctcct tcgctccaat acccctaaac tcgcacctat 120
ctcttctctt gttegtcttc aagttcaaaa gtcgagaaac tatggtaccg tatcatctgt 180
tcctctctcaa gctacagaaa catcaagcac atcacctagt aaggatgtct accaagaagc 240
actcaacgca actgaacccc gcagcaattg gacaagagaa gaaatcaagg cgatctatga 300
taagccattg atggagtatt gttgggggtgc tggtagtttg cacaggaaat tccatataacc 360
tggggctatt cagatgtgta cattgttgaa catcaagacg ggtggttgct cggaggattg 420
ttcttactgc gcccaatcat cccgctacca aaccggtctc aaagcctcca aaatggtctc 480
cgtcgaatct gtctcgcag cgcgccgcag cgccaaagac aacggtagta cacgtttctg 540
catgggagcc gcgtggcgcg atatgcgtgg acgaaaaacc aatctcaaaa atgtcaaaac 600
aatggttagc gagattcgcg gaatgggtat ggaagtatgt gtcacgcttg gtatgattga 660
tgcagagcaa gctcaggaac tcaaagaagc cggctctcag gcttataatc ataattgtgga 720
tacgtcgagg gatttctatc ccaagggtat cagcaccagg acttatgatg agagattgga 780
taccattaag aatgtgagag aggccggaat caatgtttgt acgggtggaa tcctcggatt 840
aggagaaaaat aagtctgacc atattggact tttggagacg gttgctacgt tgccttcgca 900
tccggaatca tttcctgtga acatgttagt ggctatcaaa ggaacaccac tggaaggaaa 960
caagaagggtg gaatttgaga atatgttgag aatggttgcg acggctagaa tcgtcatgcc 1020
taaaaccatc gtgcgttttg cagctggaag aggagaattg agcgaggaac aacaggtctt 1080
atgtttcatg gccggagcca atgcggtttt cacaggagaa acaatgttaa ccacaccagc 1140
cgttggatgg ggtgtcgatt ccgtcgtttt caacagatgg ggattaagac ccatggaaag 1200
tttcgagggtt gaagccttga agaacgataa acctgccact actaatcagg aaataccggt 1260
agaggcaagt aaggcagaga tgccagggtac agttgcttga ttgattgttt gatttggata 1320
cccagggcgt ttggtgcgct catcatctcg agtttttgca aggagattcg aacagtggaa 1380
gtgccgttgc gccaccattg ggattggcgt atcggaactga gattgactgt gccacgaaaa 1440
tgttttgccg tatcgtgtgt tgcatctcgt tgggaattta gcgttggttg ttttggtttt 1500
ggttttgttt gatgtgagag aatgattgtt tagaagggga gaatgtatat acggaacagt 1560

Ile Gly Leu Leu Glu Thr Val Ala Thr Leu Pro Ser His Pro Glu Ser
275 280 285

Phe Pro Val Asn Met Leu Val Ala Ile Lys Gly Thr Pro Leu Glu Gly
290 295 300

Asn Lys Lys Val Glu Phe Glu Asn Met Leu Arg Met Val Ala Thr Ala
305 310 315 320

Arg Ile Val Met Pro Lys Thr Ile Val Arg Leu Ala Ala Gly Arg Gly
325 330 335

Glu Leu Ser Glu Glu Gln Gln Val Leu Cys Phe Met Ala Gly Ala Asn
340 345 350

Ala Val Phe Thr Gly Glu Thr Met Leu Thr Thr Pro Ala Val Gly Trp
355 360 365

Gly Val Asp Ser Val Val Phe Asn Arg Trp Gly Leu Arg Pro Met Glu
370 375 380

Ser Phe Glu Val Glu Ala Leu Lys Asn Asp Lys Pro Ala Thr Thr Asn
385 390 395 400

Thr Glu Ile Pro Val Glu Ala Ser Lys Ala Glu Met Pro Gly Thr Val
405 410 415

Ala

<210> 31
<211> 1032
<212> DNA
<213> Triticum aestivum

<400> 31
gcacgagaga tgccgtccta gaagcagcaa aaaaggcaaa ggaggctggg agcaccgat 60
tttgcattggg agccgcatgg agagagacaa ttggcaggaa aacaaatttc aaccagattc 120
ttgaatatgt caaggacata agaggtatgg gcatggagggt ctggttcacc ctgggcatgc 180
tagagaaaca acaagctgaa gaactcaaga aggctggact tacagcttat aatcataacc 240
tagatacatc aagagaatat taccccaaca ttatttctac aagatcgtac gatgatagat 300
tacagactct tcagcatgtc cgtgaagctg gaataagcgt ctgctcagggt ggaattattg 360
gtcttgagaga ggcggaggaa gaccgtgtag ggctgttgca tacactggcc actttgcaa 420
cacaccacaga gagcgttcct atcaatgcat tgattgctgt caaaggcacg cctcttcagg 480
atcagaagcc tgtagagata tgggaaatga tccgcatgat tgccagcgca cggatttgtga 540
tgccaaaggc aatggtgaga ctttcggcag ggagagtacg gttttccatg ccagaacaag 600
ctctctgctt tctcgtggtg gccaactcga tcttcgcccgg tgaagagctc ctgacaactg 660
cgaacaatga ctttgatgag gaccaggcaa tgttcaagat ccttggcctg attcccaagg 720
ctccaaactt tggcgtatga gaggtcatgg tagcagcacc cacggagaga tgtgagcaag 780
ccgctttgat gtaaaatgtc ggtatagatt ctcgagacca catccggtgc aaaactggca 840
ccattatctc cacctagagt tttgtactgt agagatcatg acattttata gtaacttcag 900
attcatcgaa ataaaatagg gggttctctg caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aa 1032

<210> 32
<211> 263
<212> PRT
<213> Triticum aestivum

<400> 32

Thr Arg Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly
1 5 10 15

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
20 25 30

Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly
35 40 45

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln
50 55 60

Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
65 70 75 80

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr
85 90 95

Asp Asp Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser
100 105 110

Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
115 120 125

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
130 135 140

Val Pro Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp
145 150 155 160

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala
165 170 175

Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
180 185 190

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
195 200 205

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
210 215 220

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
225 230 235 240

Pro Asn Phe Gly Asp Glu Glu Val Met Val Ala Ala Pro Thr Glu Arg
245 250 255

Cys Glu Gln Ala Ala Leu Met
260

<210> 33

<211> 378

<212> PRT

<213> Arabidopsis thaliana

<400> 33

Met Met Leu Val Arg Ser Val Phe Arg Ser Gln Leu Arg Pro Ser Val
1 5 10 15

Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met Phe Lys Thr Leu Gly
 340 345 350
 Leu Ile Pro Lys Pro Pro Ser Phe Ser Glu Asp Asp Ser Glu Ser Glu
 355 360 365
 Asn Cys Glu Lys Val Ala Ser Ala Ser His
 370 375
 <210> 34
 <211> 363
 <212> PRT
 <213> Schizosaccharomyces pombe
 <400> 34
 Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Ser Ser Ala Leu
 1 5 10 15
 Ser Leu Val Arg Asn Asn Trp Thr Arg Glu Glu Ile Gln Lys Ile Tyr
 20 25 30
 Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg
 35 40 45
 Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Leu Ser Ile
 50 55 60
 Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser
 65 70 75 80
 Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu
 85 90 95
 Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe
 100 105 110
 Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe
 115 120 125
 Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu
 130 135 140
 Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu
 145 150 155 160
 Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg
 165 170 175
 Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu
 180 185 190
 Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
 195 200 205
 Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile
 210 215 220
 His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn
 225 230 235 240

Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu
 245 250 255
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile
 260 265 270
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys
 275 280 285
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val
 290 295 300
 Phe Thr Gly Glu Lys Met Leu Thr Thr Pro Ala Val Ser Trp Asp Ser
 305 310 315 320
 Asp Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe
 325 330 335
 Glu Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro
 340 345 350
 Pro Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu
 355 360

<210> 35

<211> 375

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 35

Met Met Ser Thr Ile Tyr Arg His Leu Ser Thr Ala Arg Pro Ala Leu
 1 5 10 15

Thr Lys Tyr Ala Thr Asn Ala Ala Val Lys Ser Thr Thr Ala Ser Ser
 20 25 30

Glu Ala Ser Thr Leu Gly Ala Leu Gln Tyr Ala Leu Ser Leu Asp Glu
 35 40 45

Pro Ser His Ser Trp Thr Lys Ser Gln Leu Lys Glu Ile Tyr His Thr
 50 55 60

Pro Leu Leu Glu Leu Thr His Ala Ala Gln Leu Gln His Arg Lys Trp
 65 70 75 80

His Asp Pro Thr Lys Val Gln Leu Cys Thr Leu Met Asn Ile Lys Ser
 85 90 95

Gly Gly Cys Ser Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser Arg Asn
 100 105 110

Asp Thr Gly Leu Lys Ala Glu Lys Met Val Lys Val Asp Glu Val Ile
 115 120 125

Lys Glu Ala Glu Glu Ala Lys Arg Asn Gly Ser Thr Arg Phe Cys Leu
 130 135 140

Gly Ala Ala Trp Arg Asp Met Lys Gly Arg Lys Ser Ala Met Lys Arg
 145 150 155 160

Ile	Gln	Glu	Met	Val	Thr	Lys	Val	Asn	Asp	Met	Gly	Leu	Glu	Thr	Cys
165								170				175			
Val	Thr	Leu	Gly	Met	Val	Asp	Gln	Asp	Gln	Ala	Lys	Gln	Leu	Lys	Asp
180								185				190			
Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Ile	Asp	Thr	Ser	Arg	Glu	His
195								200				205			
Tyr	Ser	Lys	Val	Ile	Thr	Thr	Arg	Thr	Tyr	Asp	Asp	Arg	Leu	Gln	Thr
210								215				220			
Ile	Lys	Asn	Val	Gln	Glu	Ser	Gly	Ile	Lys	Ala	Cys	Thr	Gly	Gly	Ile
225								230				235			
Leu	Gly	Leu	Gly	Glu	Ser	Glu	Asp	Asp	His	Ile	Gly	Phe	Ile	Tyr	Thr
245								250				255			
Leu	Ser	Asn	Met	Ser	Pro	His	Pro	Glu	Ser	Leu	Pro	Ile	Asn	Arg	Leu
260								265				270			
Val	Ala	Ile	Lys	Gly	Thr	Pro	Met	Ala	Glu	Glu	Leu	Ala	Asp	Pro	Lys
275								280				285			
Ser	Lys	Lys	Leu	Gln	Phe	Asp	Glu	Ile	Leu	Arg	Thr	Ile	Ala	Thr	Ala
290								295				300			
Arg	Ile	Val	Met	Pro	Lys	Ala	Ile	Ile	Arg	Leu	Ala	Ala	Gly	Arg	Tyr
305								310				315			
Thr	Met	Lys	Glu	Thr	Glu	Gln	Phe	Val	Cys	Phe	Met	Ala	Gly	Cys	Asn
325								330				335			
Ser	Ile	Phe	Thr	Gly	Lys	Lys	Met	Leu	Thr	Thr	Met	Cys	Asn	Gly	Trp
340								345				350			
Asp	Glu	Asp	Lys	Ala	Met	Leu	Ala	Lys	Trp	Gly	Leu	Gln	Pro	Met	Glu
355								360				365			
Ala	Phe	Lys	Tyr	Asp	Arg	Ser									
370								375							

<210>	36
<211>	12
<212>	PRT
<213>	